CLAIM AMENDMENTS

1. (previously presented) An isolated genomic nucleic acid molecule, said nucleic acid molecule obtainable from human chromosome 7 consisting of a nucleotide sequence selected from the group consisting of:

(a) a nucleic acid molecule of SEQ ID NO:8 which includes sequence encoding a polypeptide that has human adipocyte enhancer binding protein 1 activity;

(b) a fragment of (a) comprising at least nucleotides 1301-10893 of SEQ ID NO:8 which encodes a polypeptide having human adipocyte enhancer binding protein 1 activity and

(c) a nucleic acid molecule which is a complement of the polynucleotides specified in (a)-(b).

2. (previously presented) A nucleic acid construct comprising the nucleic acid molecule of claim 1.

3. (previously presented) An expression vector comprising the nucleic acid molecule of claim 1.

4. (original) A recombinant host cell comprising the nucleic acid molecule of claim 1.

Claim 5 (canceled)

6. (currently amended) A method for obtaining human adipocyte enhancer binding protein 1 comprising:

(a) culturing the recombinant host cell of claim 4 under conditions that provide for the expression of said ~~polypeptide~~ human adipocyte enhancer binding protein 1 and

(b) recovering said expressed human adipocyte enhancer binding protein 1 ~~polypeptide~~.

Claim 7 (canceled)

8. (withdrawn) An isolated nucleic acid molecule consisting of a fragment of the nucleic acid molecule of claim 1, said fragment comprising at least 20 contiguous nucleotides identical to an intron region of SEQ ID NO:8.

9. (canceled)

10. (previously presented) A composition comprising the nucleic acid molecule of claim 1 and a carrier.

11. (withdrawn) A composition comprising the nucleic acid molecule of claim 8 and a carrier.

Claims 12-13 (canceled)

14. (withdrawn-currently amended) A kit comprising ~~the~~ one or more nucleic acid molecules of claim 8.

15. (withdrawn-currently amended) The kit according to claim 14, in which one or more of the ~~polynucleotide~~ nucleic acid molecules ~~is~~ are optionally labeled with a detectable substance.

Claims 16-24 (canceled)

25. (withdrawn-currently amended) A method of identifying ~~variants~~ a nucleotide sequence variant of SEQ ID NO: 8 or its complementary sequence comprising
(a) isolating genomic DNA from a subject and
(b) determining the presence or absence of a variant in said genomic DNA using ~~the~~ a nucleic acid molecule ~~of~~ comprising at least 20 contiguous nucleotides of an intron region of SEQ ID NO:8 or its complementary sequence~~claim 8~~.

26. (withdrawn-currently amended) A method for detecting the presence or absence of a non-coding nucleic acid sequence specific to the nucleic acid molecule of claim 1 in a sample, said

method comprising contacting a sample with a nucleic acid molecule ~~of~~ comprising at least 20 contiguous nucleotides ~~which hybridizes at high stringency to a non-coding region specific to~~ of an intron region of ~~said nucleic acid molecule~~ SEQ ID NO:8 or its complementary sequence.

27. (withdrawn) A method of identifying a nucleotide sequence variant of SEQ ID NO:8 or its complementary sequence comprising

(a) isolating genomic DNA from a subject, and

(b) determining the presence or absence of a nucleotide sequence variation in said genomic DNA by comparing the nucleotide acid sequence of SEQ ID NO:8 with the nucleotide sequence of the isolated genomic DNA and establishing if and where a difference occurs between the two nucleic acid sequences thereby identifying a nucleotide sequence variant of SEQ ID NO:8 or its complement.

28. (withdrawn) The method of claim 27, wherein the presence or absence of a nucleotide sequence variation is determined in a 5'-noncoding region, 3'-noncoding region or intron region of SEQ ID NO: 8 or its complementary sequence.

29. (withdrawn-currently amended) A method of detecting the presence or absence of a polynucleotide having the nucleic acid sequence set forth depicted in SEQ ID NO:8 or its complementary sequence in a sample, said method comprising

(a) contacting the sample with a nucleic acid molecule comprising at least 20 contiguous nucleotides of an intron region of SEQ ID NO:8 or its complementary sequence ~~polynucleotide of claim 8~~ under stringent hybridization conditions and

(b) determining whether the ~~polynucleotide~~ nucleic acid molecule in (a) binds to a polynucleotide ~~sequence~~ in the sample, wherein binding of a polynucleotide of the sample to ~~a~~ the nucleic acid molecule of (a) ~~polynucleotide of claim 8~~ detects the presence of a polynucleotide comprising SEQ ID NO:8.

30. (withdrawn-currently amended) The isolated nucleic acid molecule of claim 8, wherein said intron region is selected from the group consisting of the sequence of nucleotides between positions 9015-10,641, 8122-8672, 7932-8049, 7754-7859, 7554-7628, 6662-7475, 6452-6583,

6273-6375, 5456-6218, 535305434, 4834-5211, 4647-4749, 4407-4502, 4053-4319, 3707-3929, 3418-3508, 3001-3237, 2570-2650, 2305-2425 and 1967-2208.

31. (currently amended) An isolated nucleic acid molecule consisting of a fragment of the nucleic acid molecule of claim 1 said fragment comprising at least 20 contiguous nucleotides of an intron region of SEQ ID NO:8 or its complementary sequence. ~~The isolated nucleic acid molecule of claim 8~~, wherein said intron region is the sequence of nucleotides between positions 9015-10,641.

32. (new) An isolated nucleic acid molecule consisting of a fragment of the nucleic acid molecule of claim 1, said fragment comprising at least 20 contiguous nucleotides identical to an intron region of SEQ ID NO:8, wherein said intron region is the sequence of nucleotides between positions 8122-8672**,** 6662-7475, 5456-6218, 4834-5211, and 4053-4319 of SEQ ID NO:8.